

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: LI, Limin
COHEN, Stanley N
- (ii) TITLE OF INVENTION: MAMMALIAN TUMOR SUSCEPTIBILITY GENES AND
THEIR USES
- (iii) NUMBER OF SEQUENCES: 20
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
 - (B) STREET: 4 Embarcadero Center, Suite 1200
 - (C) CITY: San Francisco
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 94111-1
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: SHERWOOD, Pamela J.
 - (B) REGISTRATION NUMBER: 36,677
 - (C) REFERENCE/DOCKET NUMBER: A62783-1/BIR/PJS
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 415-781-1989
 - (B) TELEFAX: 415-398-3249
 - (C) TELEX: 910 277299

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1448 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 61..1203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCCCTCTGCC TGTGGGGACG GAGGAGCGCG CCATGGCTGT CCGAGAGTCA GCTGAAGAAG

ATG ATG TTT AAG TAC AAA TAT AGA GAT CTA ACC GTC CGT CAA ACT GTC Met Met Ser Lys Tyr Lys Tyr Arg Asp Leu Thr Val Arg Gln Thr Val 1 5 10 15	108
AAT GTC ATC GCT ATG TAC AAA GAT CTC AAA CCT GTA TTG GAT TCA TAT Asn Val Ile Ala Met Tyr Lys Asp Leu Lys Pro Val Leu Asp Ser Tyr 20 25 30	156
GTT TTT AAT GAT GGC AGT TCC AGG GAG CTG GTG AAC CTC ACT GGT ACA Val Phe Asn Asp Gly Ser Ser Arg Glu Leu Val Asn Leu Thr Gly Thr 35 40 45	204
ATC CCA GTG CGT TAT CGA GGT AAT ATA TAT AAT ATT CCA ATA TGC CTG Ile Pro Val Arg Tyr Arg Gly Asn Ile Tyr Asn Ile Pro Ile Cys Leu 50 55 60	252
TGG CTG CTG GAC ACA TAC CCA TAT AAC CCC CCT ATC TGT TTT GTT AAG Trp Leu Leu Asp Thr Tyr Pro Tyr Asn Pro Pro Ile Cys Phe Val Lys 65 70 75 80	300
CCT ACT AGT TCA ATG ACT ATT AAA ACA GGA AAG CAT GTG GAT GCA AAT Pro Thr Ser Ser Met Thr Ile Lys Thr Gly Lys His Val Asp Ala Asn 85 90 95	348
GGG AAA ATC TAC CTA CCT TAT CTA CAT GAC TGG AAA CAT CCA CGG TCA Gly Lys Ile Tyr Leu Pro Tyr Leu His Asp Trp Lys His Pro Arg Ser 100 105 110	396
GAG TTG CTG GAG CTT ATT CAA ATC ATG ATT GTG ATA TTT GGA GAG GAG Glu Leu Leu Glu Leu Ile Gln Ile Met Ile Val Ile Phe Gly Glu Glu 115 120 125	444
CCT CCA GTG TTC TCC CGG CCT ACT GTT TCT GCA TCC TAC CCA CCA TAC Pro Pro Val Phe Ser Arg Pro Thr Val Ser Ala Ser Tyr Pro Pro Tyr 130 135 140	492
ACA GCA ACA GGG CCA CCA AAT ACC TCC TAC ATG CCA GGC ATG CCA AGT Thr Ala Thr Gly Pro Pro Asn Thr Ser Tyr Met Pro Gly Met Pro Ser 145 150 155 160	540
GGA ATC TCT GCA TAT CCA TCT GGA TAC CCT CCC AAC CCC AGT GGT TAT Gly Ile Ser Ala Tyr Pro Ser Gly Tyr Pro Pro Asn Pro Ser Gly Tyr 165 170 175	588
CCT GGC TGT CCT TAC CCA CCT GCT GGC CCA TAC CCT GCC ACA ACA AGC Pro Gly Cys Pro Tyr Pro Pro Ala Gly Pro Tyr Pro Ala Thr Thr Ser 180 185 190	636
TCA CAG TAC CCT TCC CAG CCT CCT GTG ACC ACT GTT GGT CCC AGC AGA Ser Gln Tyr Pro Ser Gln Pro Pro Val Thr Thr Val Gly Pro Ser Arg 195 200 205	684
GAT GGC ACA ATC AGT GAG GAC ACT ATC CGT GCA TCT CTC ATC TCA GCA Asp Gly Thr Ile Ser Glu Asp Thr Ile Arg Ala Ser Leu Ile Ser Ala 210 215 220	732
GTC AGT GAC AAA CTG AGA TGG CGG ATG AAG GAG GAA ATG GAT GGT GCC Val Ser Asp Lys Leu Arg Trp Arg Met Lys Glu Glu Met Asp Gly Ala 225 230 235 240	780
CAG GCA GAG CTT AAT GCC TTG AAA CGA ACA GAG GAA GAT CTG AAA AAA Gln Ala Glu Leu Asn Ala Leu Lys Arg Thr Glu Glu Asp Leu Lys Lys	828

245

250

255

GGC CAC CAG AAA CTG GAA GAG ATG GTC ACC CGC TTA GAT CAA GAA GTA 876
 Gly His Gln Lys Leu Glu Glu Met Val Thr Arg Leu Asp Gln Glu Val
 260 265 270

GCT GAA GTT GAT AAA AAC ATA GAA CTT TTG AAA AAG AAG GAT GAA GAA 924
 Ala Glu Val Asp Lys Asn Ile Glu Leu Leu Lys Lys Lys Asp Glu Glu
 275 280 285

CTA AGT TCT GCT CTG GAG AAA ATG GAA AAT CAA TCT GAA AAT AAT GAT 972
 Leu Ser Ser Ala Leu Glu Lys Met Glu Asn Gln Ser Glu Asn Asn Asp
 290 295 300

ATT GAT GAA GTT ATC ATT CCC ACA GCC CCA CTG TAT AAA CAG ATT CTA 1020
 Ile Asp Glu Val Ile Ile Pro Thr Ala Pro Leu Tyr Lys Gln Ile Leu
 305 310 315 320

AAT CTG TAT GCA GAG GAA AAT GCT ATT GAA GAC ACT ATC TTT TAC CTT 1068
 Asn Leu Tyr Ala Glu Glu Asn Ala Ile Glu Asp Thr Ile Phe Tyr Leu
 325 330 335

GGA GAA GCT TTG CGG CGG GGA GTC ATA GAC CTG GAT GTG TTC CTG AAA 1116
 Gly Glu Ala Leu Arg Arg Gly Val Ile Asp Leu Asp Val Phe Leu Lys
 340 345 350

CAC GTC CGC CTC CTG TCC CGT AAA CAG TTC CAG CTA AGG GCA CTA ATG 1164
 His Val Arg Leu Leu Ser Arg Lys Gln Phe Gln Leu Arg Ala Leu Met
 355 360 365

CAA AAG GCA AGG AAG ACT GCG GGC CTT AGT GAC CTC TAC TGACATGTGC 1213
 Gln Lys Ala Arg Lys Thr Ala Gly Leu Ser Asp Leu Tyr
 370 375 380

TGTCAGCTGG AGACCGACCT CTCCGTAAAG CATTCTTTTC TTCTTCTTTT TCTCATCAGT 1273

AGAACCCACA ATAAGTTATT GCAGTTTATC ATTCAAGTGT TAAATATTTT GAATCAATAA 1333

TATATTTTCT GTTTCCTTTG GGTAAAACT GGCTTTTATT AATGCACTTT CTACCCTCTG 1393

TAAGCGTCTG TGCTGTGCTG GGACTGACTG GGCTAAATAA AATTGTTGC ATAAA 1448

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Met Ser Lys Tyr Lys Tyr Arg Asp Leu Thr Val Arg Gln Thr Val
 1 5 10 15

Asn Val Ile Ala Met Tyr Lys Asp Leu Lys Pro Val Leu Asp Ser Tyr
 20 25 30

Val Phe Asn Asp Gly Ser Ser Arg Glu Leu Val Asn Leu Thr Gly Thr
 35 40 45

Ile Pro Val Arg Tyr Arg Gly Asn Ile Tyr Asn Ile Pro Ile Cys Leu
 50 55 60
 Trp Leu Leu Asp Thr Tyr Pro Tyr Asn Pro Pro Ile Cys Phe Val Lys
 65 70 75 80
 Pro Thr Ser Ser Met Thr Ile Lys Thr Gly Lys His Val Asp Ala Asn
 85 90 95
 Gly Lys Ile Tyr Leu Pro Tyr Leu His Asp Trp Lys His Pro Arg Ser
 100 105 110
 Glu Leu Leu Glu Leu Ile Gln Ile Met Ile Val Ile Phe Gly Glu Glu
 115 120 125
 Pro Pro Val Phe Ser Arg Pro Thr Val Ser Ala Ser Tyr Pro Pro Tyr
 130 135 140
 Thr Ala Thr Gly Pro Pro Asn Thr Ser Tyr Met Pro Gly Met Pro Ser
 145 150 155 160
 Gly Ile Ser Ala Tyr Pro Ser Gly Tyr Pro Pro Asn Pro Ser Gly Tyr
 165 170 175
 Pro Gly Cys Pro Tyr Pro Pro Ala Gly Pro Tyr Pro Ala Thr Thr Ser
 180 185 190
 Ser Gln Tyr Pro Ser Gln Pro Pro Val Thr Thr Val Gly Pro Ser Arg
 195 200 205
 Asp Gly Thr Ile Ser Glu Asp Thr Ile Arg Ala Ser Leu Ile Ser Ala
 210 215 220
 Val Ser Asp Lys Leu Arg Trp Arg Met Lys Glu Glu Met Asp Gly Ala
 225 230 235 240
 Gln Ala Glu Leu Asn Ala Leu Lys Arg Thr Glu Glu Asp Leu Lys Lys
 245 250 255
 Gly His Gln Lys Leu Glu Glu Met Val Thr Arg Leu Asp Gln Glu Val
 260 265 270
 Ala Glu Val Asp Lys Asn Ile Glu Leu Leu Lys Lys Lys Asp Glu Glu
 275 280 285
 Leu Ser Ser Ala Leu Glu Lys Met Glu Asn Gln Ser Glu Asn Asn Asp
 290 295 300
 Ile Asp Glu Val Ile Ile Pro Thr Ala Pro Leu Tyr Lys Gln Ile Leu
 305 310 315 320
 Asn Leu Tyr Ala Glu Glu Asn Ala Ile Glu Asp Thr Ile Phe Tyr Leu
 325 330 335
 Gly Glu Ala Leu Arg Arg Gly Val Ile Asp Leu Asp Val Phe Leu Lys
 340 345 350
 His Val Arg Leu Leu Ser Arg Lys Gln Phe Gln Leu Arg Ala Leu Met
 355 360 365
 Gln Lys Ala Arg Lys Thr Ala Gly Leu Ser Asp Leu Tyr
 370 375 380

(i) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 120..1259

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAAGGGGGTG TGCATTGTG TGGGACGGTC TGGGGCAGCC ACAGCGGCTG ACCNCNTNGC 60
CTGCGGGGAA GGGAGTCGCC AGGGCCCGTC ATCGGGTGTC GGAGAGCCAG CTCAAGAAAA 120
TGGTGTCCAA GTACAAATAC AGAGACCTAA CTGTACGTGA AACTGTCAAT GTTATTACTC 180
TATACAAAGA TCTCAAACCT GTTTTGGATT CATATGTTTT TAACGATGGC AGTTCAGGG 240
AACTAATGAA CCTCACTGGA ACAATCCCTG TGCCTTATAG AGGTAATACA TACAATATTC 300
CAATATGCCT ATGGCTACTG GACACATACC CATATAATCC CCCTATCTGT TTTGTTAAGC 360
CTACTAGTTC AATGACTATT AAAACAGGAA AGCATGTTGA TGCAAATGGG AAGATATATC 420
TTCCTTATCT ACATGAATGG AAACACCCAC AGTCAGACTT GTTGGGGCTT ATTCAGGTCA 480
TGATTGTGGT ATTTGGAGAT GAACCTCCAG TCTTCTCTCG TCCTATTTTCG GCATCCTATC 540
CGCCATACCA GGCAACGGGG CCACCAAATA CTTCTTACAT GCCAGGCATG CCAGGTGGAA 600
TCTCTCCATA CCCATCCGGA TACCCTCCCA ATCCCAGTGG TTACCCAGGC TGTCCTTACC 660
CACCTGGTGG TCCATATCCT GCCACAACAA GTTCTCAGTA CCCTTCTCAG CCTCCTGTGA 720
CCACTGTTGG TCCCAGTAGG GATGGCACAA TCAGCGAGGA CACCATCCGA GCCTCTCTCA 780
TCTCTGCGGT CAGTGACAAA CTGAGATGGC GGATGAAGGA GGAAATGGAT CGTGCCCAGG 840
CAGAGCTCAA TGCCTTGAAA CGAACAGAAG AAGACCTGAA AAAGGGTCAC CAGAAACTGG 900
AAGAGATGGT TACCCGTTTA GATCAAGAAG TAGCCGAGGT TGATAAAAAC ATAGAACTTT 960
TGAAAAAGAA GGATGAAGAA CTCAGTTCTG CTCTGGAAAA AATGGAAAAT CAGTCTGAAA 1020
ACAATGATAT CGATGAAGTT ATCATCCCA CAGCTCCCTT ATACAAACAG ATCCTGAATC 1080
TGTATGCAGA AGAAAACGCT ATTGAAGACA CTATCTTTTA CTTGGGAGAA GCCTTGAGAA 1140
GGGGCGTGAT AGACCTGGAT GTCTTCCTGA AGCATGTACG TCTTCTGTCC CGTAAACAGT 1200
TCCAGCTGAG GGCACATAATG CAAAAGCAA GAAAGACTGC CGGTCTCAGT GACCTCTACT 1260
GACTTCTCTG ATACCAGCTG GAGGTTGAGC TCTTCTTAAA GTATTCTTCT CTTCTTTTA 1320
TCACTAGGTG CCCAGAATAA GTTATTGCAG TTTATCATTC AAGTGTAATAA TATTTTGAAT 1380

CAATAATATA TTTTCTGTTT TCTTTTGGTA AAGACTGGCT TTTATTAATG CACTTTCTAT 1440

CCTCTGTAAA CTTTTTGTGC TGAATGTTGG GACTGCTAAA TAAAATTTGT TTTT 1494

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 380 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Val Ser Lys Tyr Lys Tyr Arg Asp Leu Thr Val Arg Glu Thr Val
1 5 10 15

Asn Val Ile Thr Leu Tyr Lys Asp Leu Lys Pro Val Leu Asp Ser Tyr
20 25 30

Val Phe Asn Asp Gly Ser Ser Arg Glu Leu Met Asn Leu Thr Gly Thr
35 40 45

Ile Pro Val Pro Tyr Arg Gly Asn Thr Tyr Asn Ile Pro Ile Cys Leu
50 55 60

Trp Leu Leu Asp Thr Tyr Pro Tyr Asn Pro Pro Ile Cys Phe Val Lys
65 70 75 80

Pro Thr Ser Ser Met Thr Ile Lys Thr Gly Lys His Val Asp Ala Asn
85 90 95

Gly Lys Ile Tyr Leu Pro Tyr Leu His Glu Trp Lys His Pro Gln Ser
100 105 110

Asp Leu Leu Gly Leu Ile Gln Val Met Ile Val Val Phe Gly Asp Glu
115 120 125

Pro Pro Val Phe Ser Arg Pro Ile Ser Ala Ser Tyr Pro Pro Tyr Gln
130 135 140

Ala Thr Gly Pro Pro Asn Thr Ser Tyr Met Pro Gly Met Pro Gly Gly
145 150 155 160

Ile Ser Pro Tyr Pro Ser Gly Tyr Pro Pro Asn Pro Ser Gly Tyr Pro
165 170 175

Gly Cys Pro Tyr Pro Pro Gly Gly Pro Tyr Pro Ala Thr Thr Ser Ser
180 185 190

Gln Tyr Pro Ser Gln Pro Pro Val Thr Thr Val Gly Pro Ser Arg Asp
195 200 205

Gly Thr Ile Ser Glu Asp Thr Ile Arg Ala Ser Leu Ile Ser Ala Val
210 215 220

Ser Asp Lys Leu Arg Trp Arg Met Lys Glu Glu Met Asp Arg Ala Gln
225 230 235 240

Ala Glu Leu Asn Ala Leu Lys Arg Thr Glu Glu Asp Leu Lys Lys Gly
245 250 255

His Gln Lys Leu Glu Glu Met Val Thr Arg Leu Asp Gln Glu Val Ala
 260 265 270
 Glu Val Asp Lys Asn Ile Glu Leu Leu Lys Lys Lys Asp Glu Glu Leu
 275 280 285
 Ser Ser Ala Leu Glu Lys Met Glu Asn Gln Ser Glu Asn Asn Asp Ile
 290 295 300
 Asp Glu Val Ile Ile Pro Thr Ala Pro Leu Tyr Lys Gln Ile Leu Asn
 305 310 315 320
 Leu Tyr Ala Glu Glu Asn Ala Ile Glu Asp Thr Ile Phe Tyr Leu Gly
 325 330 335
 Glu Ala Leu Arg Arg Gly Val Ile Asp Leu Asp Val Phe Leu Lys His
 340 345 350
 Val Arg Leu Leu Ser Arg Lys Gln Phe Gln Leu Arg Ala Leu Met Gln
 355 360 365
 Lys Ala Arg Lys Thr Ala Gly Leu Ser Asp Leu Tyr
 370 375 380

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

His Thr His Leu Ala Met Asx Asp Ala
 1 5

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 10 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Phe Xaa Asn Gly Ala Leu Glx Cys Tyr Ser
 1 5 10

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AGGUCAUGAU UGUGGUAUUU GGAGAUG

27

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CAUCUCCAAA UACCACAAUC AUGACCU

27

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CAUCAUCAUC AUGAGGTGGC TTATGAGTAT TTCTCCAG

39

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CUACUACUAC UACACCTTTT GAGCAAGTTC AGCCTGGTT

39

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTGATACCAG CTGGAGGTTG AGCTCTTC

28

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATTAGCAGT CCCAACATTC AGCACAAA

28

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGACCGACC TCTCCGTAAA GCATTCTT

28

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TAGCCCAGTC AGTCCCAGCA CAGCACAG

28

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 28 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

ATTTAGCAGT CCCAACATTC AGCACAAA

28

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GTCTTCTGGG TGGCAGTGAT GGCAT

25

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CGGGTGTCGG AGAGCCAGCT CAAGAAA

27

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCTTACCCAC CTGGTGGTCC ATATCCTG

28

- (2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CCTCCAGCTG GTATCAGAGA AGTCGT

26

- (2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Primer"

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CACAGTCAGA CTTGTTGGGG CTTATTC

27